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0625

H6

ENTERED

see page 6



OIPE

RAW SEQUENCE LISTING

DATE: 06/20/2002

PATENT APPLICATION: US/10/067,534

TIME: 17:36:53

Input Set : A:\006602-113.ST25.txt

Output Set: N:\CRF3\06202002\J067534.raw

3 <110> APPLICANT: Essenberg, Margaret K.
 4 Chen, Xiao-Ya
 5 Luo, Ping
 6 Wang, Yan-Hong
 8 <120> TITLE OF INVENTION: cDNA Clone of (+)-Delta-Cadinene-8-Hydroxylase Gene from
 Cotton Plants
 10 <130> FILE REFERENCE: 006602-113
 12 <140> CURRENT APPLICATION NUMBER: US 10/067,534
 13 <141> CURRENT FILING DATE: 2002-02-07
 15 <150> PRIOR APPLICATION NUMBER: US 60/267,160
 16 <151> PRIOR FILING DATE: 2001-02-07
 18 <160> NUMBER OF SEQ ID NOS: 19
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1933
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Gossypium arboreum
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 29 atttcttgggt ttctctcaag aaggaagaag atgttgcaaa tagctttcag ctctgattca 120
 30 tggctgttga ctgctagcaa ccagaaagat ggaatgttgt tcccagtagc ttgttcattt 180
 31 ttggtagcca tattgggaat ttactgttg cactatgga ccataaggaa gccaaagaaa 240
 32 gacatcgccc cattaccgcc gggtccccgt gggttgccaa tagtgggata tcttccatat 300
 33 cttgggaactg ataactctca cttggtgttt acagatttgg ctgcagctta cgtgccatc 360
 34 tacaagcttt ggctaggaaa caaattatgc gtagtcattt gctcggcacc actggcgaaa 420
 35 gaagtgggtc gtgacaacga catcacattt tctgaaagg atcctccgt ttgtgcaag 480
 36 attattacct ttggcctcaa tgatattgta tttgattctt acagtagtcc agattggaga 540
 37 atgaagagaa aagtgttgt acgtgaaatg cttagccata gtagcattaa agcttggtat 600
 38 ggtctaagga gggaacaagt gcttaaaggc gtacaaaatg ttgctcaaag tgcaggcaag 660
 39 ccaattgatt ttggtgaaac ggcattttta acatcaatca atgcgatgat gagcatgctg 720
 40 tggggtggca aacagggagg agagcggaaa ggggccgacg tttggggcca atttcgagat 780
 41 ctcataaccg aactaatggt gatacttgga aaaccaaagc tttctgatat tttcccggtg 840
 42 cttgcaagggt ttgacataca gggattggag aaggaaatga ctaaaatcgt taattctttc 900
 43 gataagcttt tcaactccat gattgaagaa agagagaact ttagcaacaa attgagcaaa 960
 44 gaagatggaa aactgaaac aaaagacttc ttgcagcttc tgttggaact caagcagaag 1020
 45 aacgatagcg gaatatcgat aacaatgaat caagtcaagg ccttgctcat ggacattgtg 1080
 46 gtcggtggaa ctgatacaac atcaaccatg atggaatgga caatggctga actaattgca 1140
 47 aatcctgaag caatgaaaaa ggtgaagcaa gaaatagacg atgttgctgg ttccgatggc 1200
 48 gccgtcgatg agactcatt gcctaagttg cgctatctag atgctgcagt aaaggagacc 1260
 49 ttccgattgc acccaccgat gccactcctt gtaccocgtt gcccgggcga ctcaagcaac 1320
 50 gttggtggct atagcgtacc aaagggcacc aggtctctct taaacatttg gtgtattcag 1380
 51 agggatccac agctttggga aaatccttta gaattcaagc ctgagagggt cttgactgat 1440
 52 catgagaagc tcgattatgt aggaacgat tcccgggtaca tgccgttttg ttctggaag 1500
 53 agaattgtgt ccggagtatc tctcgggtgaa aagatgttgt attcctcctt ggcagcaatg 1560

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Input Set : A:\006602-113.ST25.txt

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54 atccatgctt atgattggaa cttggccgac ggtgaagaaa atgacttgat tggcttattt 1620
55 ggaattatta tgaagaaaaa gaagccttta attcttggtc ctacaccaag accatcaaat 1680
56 ctccagcact atatgaagta actttactat tgtattttctt ttataccact ttattgcctc 1740
57 tttgtcatgt ttaggcaaca attctaagta ataagtttgg ctatatggtg aacaataatg 1800
58 tgtttattat acatcataag caatgagctc ttcccgaccc tagggcaata caatgatact 1860
59 gtgtattaag tgaatcaac aaatctttta ttctaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
60 aaaaaaaaaa aaa 1933
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 535
64 <212> TYPE: PRT
65 <213> ORGANISM: Gossypium arboreum
67 <400> SEQUENCE: 2
68 Met Leu Gln Ile Ala Phe Ser Ser Tyr Ser Trp Leu Leu Thr Ala Ser
69 1 5 10 15
70 Asn Gln Lys Asp Gly Met Leu Phe Pro Val Ala Leu Ser Phe Leu Val
71 20 25 30
72 Ala Ile Leu Gly Ile Ser Leu Trp His Val Trp Thr Ile Arg Lys Pro
73 35 40 45
74 Lys Lys Asp Ile Ala Pro Leu Pro Pro Gly Pro Arg Gly Leu Pro Ile
75 50 55 60
76 Val Gly Tyr Leu Pro Tyr Leu Gly Thr Asp Asn Leu His Leu Val Phe
77 65 70 75 80
78 Thr Asp Leu Ala Ala Ala Tyr Gly Pro Ile Tyr Lys Leu Trp Leu Gly
79 85 90 95
80 Asn Lys Leu Cys Val Val Ile Ser Ser Ala Pro Leu Ala Lys Glu Val
81 100 105 110
82 Val Arg Asp Asn Asp Ile Thr Phe Ser Glu Arg Asp Pro Pro Val Cys
83 115 120 125
84 Ala Lys Ile Ile Thr Phe Gly Leu Asn Asp Ile Val Phe Asp Ser Tyr
85 130 135 140
86 Ser Ser Pro Asp Trp Arg Met Lys Lys Lys Val Leu Val Arg Glu Met
87 145 150 155 160
88 Leu Ser His Ser Ser Ile Lys Ala Cys Tyr Gly Leu Arg Arg Glu Gln
89 165 170 175
90 Val Leu Lys Gly Val Gln Asn Val Ala Gln Ser Ala Gly Lys Pro Ile
91 180 185 190
92 Asp Phe Gly Glu Thr Ala Phe Leu Thr Ser Ile Asn Ala Met Met Ser
93 195 200 205
94 Met Leu Trp Gly Gly Lys Gln Gly Gly Glu Arg Lys Gly Ala Asp Val
95 210 215 220
96 Trp Gly Gln Phe Arg Asp Leu Ile Thr Glu Leu Met Val Ile Leu Gly
97 225 230 235 240
98 Lys Pro Asn Val Ser Asp Ile Phe Pro Val Leu Ala Arg Phe Asp Ile
99 245 250 255
100 Gln Gly Leu Glu Lys Glu Met Thr Lys Ile Val Asn Ser Phe Asp Lys
101 260 265 270
102 Leu Phe Asn Ser Met Ile Glu Glu Arg Glu Asn Phe Ser Asn Lys Leu
103 275 280 285
104 Ser Lys Glu Asp Gly Asn Thr Glu Thr Lys Asp Phe Leu Gln Leu Leu

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Input Set : A:\006602-113.ST25.txt

Output Set: N:\CRF3\06202002\J067534.raw

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105      290      295      300
106 Leu Asp Leu Lys Gln Lys Asn Asp Ser Gly Ile Ser Ile Met Asn Gln
107 305      310      315      320
108 Val Lys Ala Leu Leu Met Asp Ile Val Val Gly Gly Thr Asp Thr Thr
109      325      330      335
110 Ser Thr Met Met Glu Trp Thr Met Ala Glu Leu Ile Ala Asn Pro Glu
111      340      345      350
112 Ala Met Lys Lys Val Lys Gln Glu Ile Asp Asp Val Val Gly Ser Asp
113      355      360      365
114 Gly Ala Val Asp Glu Thr His Leu Pro Lys Leu Arg Tyr Leu Asp Ala
115      370      375      380
116 Ala Val Lys Glu Thr Phe Arg Leu His Pro Pro Met Pro Leu Leu Val
117 385      390      395      400
118 Pro Arg Cys Pro Gly Asp Ser Ser Asn Val Gly Gly Tyr Ser Val Pro
119      405      410      415
120 Lys Gly Thr Arg Val Phe Leu Asn Ile Trp Cys Ile Gln Arg Asp Pro
121      420      425      430
122 Gln Leu Trp Glu Asn Pro Leu Glu Phe Lys Pro Glu Arg Phe Leu Thr
123      435      440      445
124 Asp His Glu Lys Leu Asp Tyr Leu Gly Asn Asp Ser Arg Tyr Met Pro
125      450      455      460
126 Phe Gly Ser Gly Arg Arg Met Cys Ala Gly Val Ser Leu Gly Glu Lys
127 465      470      475      480
128 Met Leu Tyr Ser Ser Leu Ala Ala Met Ile His Ala Tyr Asp Trp Asn
129      485      490      495
130 Leu Ala Asp Gly Glu Glu Asn Asp Leu Ile Gly Leu Phe Gly Ile Ile
131      500      505      510
132 Met Lys Lys Lys Lys Pro Leu Ile Leu Val Pro Thr Pro Arg Pro Ser
133      515      520      525
134 Asn Leu Gln His Tyr Met Lys
135      530      535
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 516
140 <212> TYPE: PRT
141 <213> ORGANISM: Arabidopsis thaliana
143 <400> SEQUENCE: 3
144 Met Ser Pro Ile Ser Asn Leu Phe Pro Asp Asn Thr Ile Asn Leu Thr
145 1      5      10      15
146 Pro Tyr Ala Ile Val Ile Leu Thr Thr Val Phe Ser Ile Leu Trp Tyr
147      20      25      30
148 Ile Phe Lys Arg Ser Pro Gln Pro Ser Leu Pro Pro Gly Pro Arg Gly
149      35      40      45
150 Leu Pro Ile Val Gly Asn Leu Pro Phe Leu Asp Pro Asp Leu His Thr
151      50      55      60
152 Tyr Phe Ala Asn Leu Ala Gln Ser His Gly Pro Ile Phe Lys Leu Asn
153 65      70      75      80
154 Leu Gly Ser Lys Leu Thr Ile Val Val Asn Ser Pro Ser Leu Ala Arg
155      85      90      95
156 Glu Ile Leu Lys Asp Gln Asp Ile Asn Phe Ser Asn Arg Asp Val Pro

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```

157          100          105          110
158 Leu Thr Gly Arg Ala Ala Thr Tyr Gly Gly Ile Asp Ile Val Trp Thr
159          115          120          125
160 Pro Tyr Gly Ala Glu Trp Arg Gln Leu Lys Lys Ile Cys Val Leu Lys
161          130          135          140
162 Leu Leu Ser Arg Lys Thr Leu Asp Ser Phe Tyr Glu Leu Arg Arg Lys
163 145          150          155          160
164 Glu Val Arg Glu Arg Thr Arg Tyr Leu Tyr Glu Gln Gly Arg Lys Gln
165          165          170          175
166 Ser Pro Val Lys Val Gly Asp Gln Leu Phe Leu Thr Met Met Asn Leu
167          180          185          190
168 Thr Met Asn Met Leu Trp Gly Gly Ser Val Lys Ala Glu Glu Met Glu
169          195          200          205
170 Ser Val Gly Thr Glu Phe Lys Gly Val Ile Ser Glu Ile Thr Arg Leu
171          210          215          220
172 Leu Ser Glu Pro His Val Ser Asp Phe Phe Pro Trp Leu Ala Arg Phe
173 225          230          235          240
174 Asp Leu Gln Gly Leu Val Lys Arg Met Gly Val Cys Ala Arg Glu Leu
175          245          250          255
176 Asp Ala Val Leu Asp Arg Ala Ile Glu Gln Met Lys Pro Leu Arg Gly
177          260          265          270
178 Arg Asp Asp Asp Glu Val Lys Asp Phe Leu Gln Tyr Leu Met Lys Leu
179          275          280          285
180 Lys Asp Gln Glu Gly Asp Ser Glu Val Pro Ile Thr Ile Asn His Val
181          290          295          300
182 Lys Ala Leu Ile Thr Asp Met Val Val Gly Gly Thr Asp Thr Ser Thr
183 305          310          315          320
184 Asn Thr Ile Glu Phe Ala Met Ala Glu Leu Met Ser Asn Pro Glu Leu
185          325          330          335
186 Ile Lys Arg Ala Gln Glu Glu Leu Asp Glu Val Val Gly Lys Asp Asn
187          340          345          350
188 Ile Val Glu Glu Ser His Ile Thr Arg Leu Pro Tyr Ile Leu Ala Ile
189          355          360          365
190 Met Lys Glu Thr Leu Arg Leu His Pro Thr Leu Pro Leu Leu Val Pro
191          370          375          380
192 His Arg Pro Ala Glu Asn Thr Val Val Gly Gly Tyr Thr Ile Pro Lys
193 385          390          395          400
194 Asp Thr Lys Ile Phe Val Asn Val Trp Ser Ile Gln Arg Asp Pro Asn
195          405          410          415
196 Val Trp Glu Asn Pro Thr Glu Phe Arg Pro Glu Arg Phe Ile Asp Asn
197          420          425          430
198 Asn Ser Cys Asp Phe Thr Gly Ala Asn Tyr Ser Tyr Phe Pro Phe Gly
199          435          440          445
200 Ser Gly Arg Arg Ile Cys Ala Gly Val Ala Leu Ala Glu Arg Met Val
201          450          455          460
202 Leu Tyr Thr Leu Ala Thr Leu Leu His Ser Phe Asp Trp Lys Ile Pro
203 465          470          475          480
204 Glu Gly His Val Leu Asp Leu Lys Glu Lys Phe Gly Ile Val Leu Lys
205          485          490          495

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```

206 Leu Lys Ile Pro Leu Val Ala Leu Pro Ile Pro Arg Phe Ser Asp Ser
207           500                      505                      510
208 Asn Leu Tyr Leu
209           515
212 <210> SEQ ID NO: 4
213 <211> LENGTH: 520
214 <212> TYPE: PRT
215 <213> ORGANISM: Arabidopsis thaliana
217 <400> SEQUENCE: 4
218 Met Ser Met Leu Ser Asn Leu Phe Pro Asp Asn Ala Ile Ser Leu Thr
219 1           5           10           15
220 Pro Tyr Ala Tyr Ala Val Leu Ile Leu Thr Ala Thr Phe Ser Ile Leu
221           20           25           30
222 Trp Tyr Ile Phe Lys Arg Ser Pro Gln Pro Pro Leu Pro Gly Pro
223           35           40           45
224 Arg Gly Leu Pro Ile Val Gly Asn Leu Pro Phe Leu Asp Pro Asp Leu
225           50           55           60
226 His Thr Tyr Glu Thr Lys Leu Ala Gln Ser His Gly Pro Ile Phe Lys
227 65           70           75           80
228 Ile Asn Leu Gly Ser Lys Leu Thr Val Val Val Asn Ser Pro Ser Leu
229           85           90           95
230 Ala Ser Glu Ile Leu Lys Asp Gln Asp Ile Asn Phe Ser Asn His Asp
231           100          105          110
232 Val Pro Leu Thr Ala Arg Ala Val Thr Tyr Gly Gly Leu Asp Leu Val
233           115          120          125
234 Trp Leu Pro Tyr Gly Ala Glu Trp Arg Met Leu Arg Lys Val Cys Ala
235           130          135          140
236 Ala Lys Leu Phe Ser Arg Lys Thr Leu Asp Ser Phe Tyr Glu Leu Arg
237 145          150          155          160
238 Arg Lys Glu Ile Arg Glu Arg Thr Arg Cys Leu Tyr Gln Lys Gly Leu
239           165          170          175
240 Glu Lys Ser Pro Val Asn Val Gly Glu Gln Leu Phe Leu Thr Met Met
241           180          185          190
242 Asn Leu Met Met Asn Met Leu Trp Gly Gly Ser Val Lys Ala Glu Asp
243           195          200          205
244 Met Glu Ser Val Gly Thr Glu Phe Lys Gly Val Ile Ser Glu Ile Thr
245           210          215          220
246 Arg Leu Leu Gly Val Pro Asn Val Ser Asp Phe Phe Pro Met Leu Ala
247 225          230          235          240
248 Arg Phe Asp Leu Gln Gly Leu Val Lys Lys Met His Leu Tyr Ala Arg
249           245          250          255
250 Asp Leu Asp Ala Ile Leu Asp Arg Ala Ile Glu Gln Met Gln Arg Leu
251           260          265          270
252 Arg Ser Arg Asp Gly Asp Asp Gly Glu Cys Lys Asp Phe Leu Gln His
253           275          280          285
254 Leu Met Lys Leu Arg Asp Gln Glu Ala Asp Ser Asp Val Pro Ile Thr
255           290          295          300
256 Met Asn His Val Lys Ala Val Leu Met Asp Met Val Val Gly Gly Thr
257 305          310          315          320

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/20/2002
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Input Set : A:\006602-113.ST25.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 17,20
Seq#:6; Xaa Pos. 4
Seq#:16; Xaa Pos. 1,5,6,7
Seq#:18; Xaa Pos. 1,3,4,6

VERIFICATION SUMMARY

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Input Set : A:\006602-113.ST25.txt

Output Set: N:\CRF3\06202002\J067534.raw

L:294 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:298 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:309 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:313 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:430 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:434 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:463 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:467 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:471 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0